SEQUENCE LISTING

(1) GENERAL INFORMATION:

   (i) APPLICANT: Mack, David H.

  (ii) TITLE OF INVENTION: COMPUTER-AIDED VISUALIZATION OF
       EXPRESSION COMPARISON

 (iii) NUMBER OF SEQUENCES: 2

  (iv) CORRESPONDENCE ADDRESS:
      (A) ADDRESSEE: Joe Liebeschuetz of Townsend and Townsend and
          Crew LLP
      (B) STREET: Two Embarcadero Center, Eighth Floor
      (C) CITY: San Francisco
      (D) STATE: CA
      (E) COUNTRY: USA
      (F) ZIP: 94111-3834

   (v) COMPUTER READABLE FORM:
      (A) MEDIUM TYPE: Floppy disk
      (B) COMPUTER: IBM PC compatible
      (C) OPERATING SYSTEM: PC-DOS/MS-DOS
      (D) SOFTWARE: PatentIn Release #1.0, Version #1.30

  (vi) CURRENT APPLICATION DATA:
      (A) APPLICATION NUMBER: US 09/020,743
      (B) FILING DATE: 09-FEB-1998
      (C) CLASSIFICATION:

 (viii) ATTORNEY/AGENT INFORMATION:
      (A) NAME: Liebeschuetz, Joe
      (B) REGISTRATION NUMBER: 37,505
      (C) REFERENCE/DOCKET NUMBER: 018547034800US

  (ix) TELECOMMUNICATION INFORMATION:
      (A) TELEPHONE: (650) 326-2400
      (B) TELEFAX: (650) 326-2422

(2) INFORMATION FOR SEQ ID NO:1:

   (i) SEQUENCE CHARACTERISTICS:
      (A) LENGTH: 2691 base pairs
      (B) TYPE: nucleic acid
      (C) STRANDEDNESS: unknown
      (D) TOPOLOGY: not relevant

  (ii) MOLECULE TYPE: DNA (genomic)

  (vi) ORIGINAL SOURCE:
      (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

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GGAGACAGAC AGACAGCTGG CAAGAGGCAG CCTGGGGGCC ACAGCTGCTT CAGCAGACCT      60

CATGGCTGAG TGAGCCTCCC CTGGGCCCAG CACCCCACCT CAGCATGGTC CAAGCCCATG     120

GGGGGCGCTC CAGAGCACAG CCGTTGACCT TGTCTTTGGG GGCAGCCATG ACCCAGCCTC     180

CGCCTGAAAA AACGCCAGCC AAGAAGCATG TGCGACTGCA GGAGAGGCGG GGCTCCAATG     240

TGGCTCTGAT GCTGGACGTT CGGTCCCTGG GGGCCGTAGA ACCCATCTGC TCTGTGAACA     300

CACCCCGGGA GGTCACCCTA CACTTTCTGC GCACTGCTGG ACACCCCTT ACCCGCTGGG      360

CCCTTCAGCG CCAGCCACCC AGCCCCAAGC AACTGGAAGA AGAATTCTTG AAGATCCCTT     420

CAAACTTTGT CAGCCCCGAA GACCTGGACA TCCCTGGCCA CGCCTCCAAG GACCGATACA     480

AGACCATCTT GCCAAATCCC CAGAGCCGTG TCTGTCTAGG CCGGGCACAG AGCCAGGAGG     540

ACGGAGATTA CATCAATGCC AACTACATCC GAGGCTATGA CGGGAAGGAG AAGGTCTACA     600

TTGCCACCCA GGGCCCCATG CCCAACACTG TGTCGGACTT CTGGGAGATG GTGTGGCAAG     660

AGGAAGTGTC CCTCATTGTC ATGCTCACTC AGCTCCGAGA GGGCAAGGAG AAATGTGTCC     720

ACTACTGGCC CACAGAAGAG GAAACCTATG GACCCTTCCA GATCCGCATC CAGGACATGA     780

AAGAGTGCCC AGAATACACT GTGCGGCAGC TCACCATCCA GTACCAGGAA GAGCGCCGGT     840

CAGTAAAGCA CATCCTCTTT TCGGCCTGGC CAGACCATCA GACACCAGAA TCAGCTGGGC     900

CCCTGCTGCG CCTAGTGGCA GAGGTGGAGG AGAGCCCGGA GACAGCCGCC CACCCCGGGC     960

CTATCGTAGT CCACTGCAGT GCAGGGATTG GCCGGACGGG CTGCTTCATC GCCACGCGAA    1020

TTGGCTGTCA ACAGCTGAAA GCCCGAGGAG AAGTGGACAT CTGGGTATT GTGTGCCAAC     1080

TGCGGCTAGA CAGAGGGGGG ATGATCCAGA CGGACGAGCA GTACCAGTTC CTGCACCACA    1140

CTTTGGCCCT GTATGCAGGC CAGCTGCCTG AGGAACCCAG CCCCTGACCC CTGCCACCCT    1200

CCGGTGGCCC AGGTGCCTAC CTCCCTCAAG CCTGGGAAGT CACAGGAAGC AGCAGCAGTA    1260

AGGACAAGGG GCCGGATTCC AGGTCTTCAA CACTGGCCAC TCCTCTGCTT CCTCTGTTGG    1320

CCCCAGATGG ACAGTAAGGG GAACCTCCAA TGTCTCTCTG AACTTAAAGA CAGGAGCTGG    1380

CATTTATGAC AGACAAAGAA AGAAGCCCAG GTGTCCTGGT GTTCTCTGAG ACACTCTTTG    1440

TGAGCTTCAG TTTCCTGTTC TATAACATGA ACATAAGTGC TTAGCTGCCA TGAGGGAAAA    1500

GTAATGAGAG AAGTTTCTAG AAGCCACTCC AGCCACTCCT TCCTGGGGCT GACAAAAGGG    1560

TGATTCCAAG ATCATCCTTC ACCCGAGGTC CTGCCCAAGC ACAGGCCAGA TGCAAGAATG    1620

GGGAAAAGTC TGGTCCTGAT CTCCAAGTCT CAACATCCTA TCAGTGACTC TGCTCCCTGA    1680

CCACACATCG GAAGGGCTGG ATGACCCCAA TCAAAAGAAA GAACAAGGAC TCTGGTTACC    1740
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CTTGCCCTCC ACCCATGTGT CATAAGAGTA GGCTACAGAG GTGACCAGGC CTGGCAGTTG    1800

AAATCTCTGG AAGAGGGAAC ATGTGGGGAC TACTCAGAGG CAAAGAGGAG CTGCTCCTGC    1860

CTCCATGGTT GCTGGCCACT CCCACCAACT ACTCTTAGGG AGGCTAAGCA GTCTCTGTTT    1920

TGCTTCCATG GCTCAAATAA TACCCTGGGT ATGCAGGACC CACTATACCT TGCATTTGCT    1980

GGTACACCTA GAGAGCTTGG CTGTTTCCAA AAACAATCAG GGTCATAACC ATCCATGCAG    2040

ACATGGAGGC TCGGCTGAAC CAGGACTCCT CACTGTCTAC CTGAGAGAAT GAGCACCCCT    2100

CATCCATCTC AGCATCAACA CAATTTCCAG GGGACCTCAG GTCTACCTCA GGACTGAACG    2160

CCACACCTCA GGATTCCTCC TCCTTGAATC TGAGACTGGC TGCCCATTCT GAGATGGGGA    2220

TGAAGGTAAG ATGCCGCATC ACCAGGCACG CCGCCCCTGA CAGCTGCCTT GATACCAGCT    2280

CTCTGTGGAA ACCCCCGAGG AGTTGGATCT GGAGAACAGC TGGGCCTCCT CACTCAGGAC    2340

TTCTCTCCTG AAGAACACGC AGTGCTAAAA CTGAGGATGA TTTCCCTAAT GCTTCTGCTT    2400

GGCCTTATGG AGGAGCTGCT CCTTCCTTAC AGCCTTGGGG ATGGACTTGC CCACACCTCC    2460

ACCTCCCCTG AGCCCTGTGA GAGGCACGAC TGTCTATGCC AATGAGGCTC GGTGGGGGGC    2520

TCTCAAGTGC CTGATCCTGC CCTGGGCTCA GAGCCAGCCC AGAGGGAAGC AACTGCACAG    2580

CCCCACAGGC CCTCCCTGGC ACTGTCCCCC CAACCCCATC TCAGAGCTCA GAGGGTACAA    2640

GCTCCAGAAC AGTAACCAAG TGGGAAAATA AAGACTTCTT GGATGACTGA C            2691
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(2) INFORMATION FOR SEQ ID NO:2:

    (i) SEQUENCE CHARACTERISTICS:
       (A) LENGTH: 360 amino acids
       (B) TYPE: amino acid
       (C) STRANDEDNESS: not relevant
       (D) TOPOLOGY: not relevant

    (ii) MOLECULE TYPE: protein

    (vi) ORIGINAL SOURCE:
       (A) ORGANISM: Homo sapiens

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

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Met Val Gln Ala His Gly Gly Arg Ser Arg Ala Gln Pro Leu Thr Leu
1               5               10              15

Ser Leu Gly Ala Ala Met Thr Gln Pro Pro Glu Lys Thr Pro Ala
            20              25              30

Lys Lys His Val Arg Leu Gln Glu Arg Arg Gly Ser Asn Val Ala Leu
        35              40              45

Met Leu Asp Val Arg Ser Leu Gly Ala Val Glu Pro Ile Cys Ser Val
    50              55              60
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Asn Thr Pro Arg Glu Val Thr Leu His Phe Leu Arg Thr Ala Gly His
65                  70              75                  80

Pro Leu Thr Arg Trp Ala Leu Gln Arg Gln Pro Pro Ser Pro Lys Gln
                85              90                  95

Leu Glu Glu Glu Phe Leu Lys Ile Pro Ser Asn Phe Val Ser Pro Glu
                100             105             110

Asp Leu Asp Ile Pro Gly His Ala Ser Lys Asp Arg Tyr Lys Thr Ile
            115             120             125

Leu Pro Asn Pro Gln Ser Arg Val Cys Leu Gly Arg Ala Gln Ser Gln
        130             135             140

Glu Asp Gly Asp Tyr Ile Asn Ala Asn Tyr Ile Arg Gly Tyr Asp Gly
145             150             155             160

Lys Glu Lys Val Tyr Ile Ala Thr Gln Gly Pro Met Pro Asn Thr Val
                165             170             175

Ser Asp Phe Trp Glu Met Val Trp Gln Glu Glu Val Ser Leu Ile Val
            180             185             190

Met Leu Thr Gln Leu Arg Glu Gly Lys Glu Lys Cys Val His Tyr Trp
        195             200             205

Pro Thr Glu Glu Glu Thr Tyr Gly Pro Phe Gln Ile Arg Ile Gln Asp
    210             215             220

Met Lys Glu Cys Pro Glu Tyr Thr Val Arg Gln Leu Thr Ile Gln Tyr
225             230             235             240

Gln Glu Glu Arg Arg Ser Val Lys His Ile Leu Phe Ser Ala Trp Pro
            245             250             255

Asp His Gln Thr Pro Glu Ser Ala Gly Pro Leu Leu Arg Leu Val Ala
        260             265             270

Glu Val Glu Glu Ser Pro Glu Thr Ala Ala His Pro Gly Pro Ile Val
    275             280             285

Val His Cys Ser Ala Gly Ile Gly Arg Thr Gly Cys Phe Ile Ala Thr
    290             295             300

Arg Ile Gly Cys Gln Gln Leu Lys Ala Arg Gly Glu Val Asp Ile Leu
305             310             315             320

Gly Ile Val Cys Gln Leu Arg Leu Asp Arg Gly Gly Met Ile Gln Thr
            325             330             335

Asp Glu Gln Tyr Gln Phe Leu His His Thr Leu Ala Leu Tyr Ala Gly
            340             345             350

Gln Leu Pro Glu Glu Pro Ser Pro
        355             360
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